# Automatic Matching of Brain Images and Brain Atlases Using Multi-Scale Fusion Algorithms

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*This paper presents a method for matching brain images, comprising a mechanism for automatic scale selection.*

In the interpretation of functional activation patterns, crucial steps concern how to relate the measurement data to an anatomical reference and how to compare the activation patterns of different individuals. As a tool in this process, a routine procedure has now been established of mapping the measurement data into a standard anatomical format (a brain atlas) and to analyse the data in this space.

For a given individual, the normal procedure for relating PET data to anatomy is to match the PET image to an NMR image by a global rigid transformation. The first standard brain format by Talairach *et al.* (1967) also included a rigid transformation complemented by rescalings of the coordinate axes to align the outer dimensions of the brain. Since then, refined approaches have been developed where a representative brain is chosen as a reference, and global linear and non-linear transformations are used for transforming individual brains to the standard brain format (Evans *et al.* 1992; Greitz *et al.* 1991; Roland and Zilles 1994). Individual brains, however, differ more than in gross anatomy, and the fine-scale sulcal structure can vary significantly between subjects.

To allow for automatic determination of local deformations, and to overcome the limitations of using manual selection of the transformation parameters, we have considered a recently developed computer vision framework for multi-scale image fusion (Bergen *et al.* 1992; Kanade and Okutomi 1994; Lindeberg 1995, 1996) and applied it to the matching of 3-D brain images.

The rationale for this approach is that local deformations will, in general, be needed if we are to align the large-scale sulcal patterns between different individuals (or functional/cytoarchitectonical areas). Moreover, routine usage requires such fusion to be at least semi-automatic. We cannot, however, expect to be able to match all fine-scale sulci and gyrii, since differences in cortical topology may make such matching impossible. A highly attractive property of the matching framework in (Lindeberg 1995, 1996) is that it comprises a mechanism for automatic scale selection. The overall matching is performed in a coarse-to-fine manner, where large-size structures are matched first. Then, if structures at finer scales (such as small-size sulci or gyrii) cannot be matched, the coarse-to-fine propagation stops and the algorithm signals that only a coarse-scale match was possible in this region. In this way, the matching scheme has the ability to signal to what extent fusion is possible in any given region.

The scheme we have implemented comprises the following main computational steps: Define subsampled scale-space representations (Lindeberg 1994) of the two images that are to be matched. Then, apply the constant-brightness assumption (Horn and Schunck 1981) between these domains, and assume that this relation holds over some region. By straightforward calculations, a direct disparity estimate can then be obtained by integrating local partial derivatives in that region (Bergen *et al.* 1992). Apply this scheme in an iterative coarse-to-fine fashion and compute a measure of uncertainty at each scale. Finally, select the disparity estimate from the scale that minimizes the uncertainty over scales (Lindeberg 1995, 1996). For more details, the reader is referred to the abovementioned sources and to (Eriksson *et al.* 1997). Important properties which can be demonstrated for this scheme are that (i) large scale structures lead to the selection of coarser scales, (ii) increasing noise level leads to the selection of coarser scales, (iii) finer scales are selected at discontinuities. In this way, the qualitative properties of this flow estimation scheme agree with the intuitive requirements we would state on a brain matching scheme, which is to match image data for which a perfect correspondence (inherently) cannot be defined at all.

Related approaches have been presented by Bajscy *et al.* (1983) and Schormann (1995) who also exploit the constant-brightness assumption while using a global regularization approach. Our approach is more similar to the work by Collins *et al.* (1995) who also perform a coarse-to-fine multi-scale matching. The main difference is that we address the problem of automatic scale selection.

To conclude, we argue that *local deformation fields* are necessary to increase the degree of alignment between anatomical and functional regions between different individuals. Specifically, when matching data between different individuals, we argue that it is essential to select the scale parameter properly, since it controls the regions over which the fusion is performed.

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